

Rod A Wing

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281 papers	40,267 citations	87 h-index	198 g-index
296 ext. papers	46,623 ext. citations	10.4 avg, IF	7.27 L-index

#	Paper	IF	Citations
281	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010 , 463, 178-83	50.4	2997
280	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
279	The map-based sequence of the rice genome. <i>Nature</i> , 2005 , 436, 793-800	50.4	2923
278	A draft sequence of the rice genome (<i>Oryza sativa</i> L. ssp. japonica). <i>Science</i> , 2002 , 296, 92-100	33.3	2591
277	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
276	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
275	Human gut microbiota in obesity and after gastric bypass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2365-70	11.5	1370
274	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
273	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
272	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018 , 557, 43-49	50.4	582
271	The <i>Ashbya gossypii</i> genome as a tool for mapping the ancient <i>Saccharomyces cerevisiae</i> genome. <i>Science</i> , 2004 , 304, 304-7	33.3	558
270	The <i>Amborella</i> genome and the evolution of flowering plants. <i>Science</i> , 2013 , 342, 1241089	33.3	546
269	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011 , 43, 101-8	36.3	502
268	Doubling genome size without polyploidization: dynamics of retrotransposition-driven genomic expansions in <i>Oryza australiensis</i> , a wild relative of rice. <i>Genome Research</i> , 2006 , 16, 1262-9	9.7	430
267	An integrated physical and genetic map of the rice genome. <i>Plant Cell</i> , 2002 , 14, 537-45	11.6	374
266	Construction and characterization of a bacterial artificial chromosome library of <i>Sorghum bicolor</i> . <i>Nucleic Acids Research</i> , 1994 , 22, 4922-31	20.1	360
265	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013 , 500, 335-9	50.4	337

264	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in <i>Gossypium</i> . <i>Genome Research</i> , 2006 , 16, 1252-61	9.7	316
263	A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (<i>Gossypium</i>). <i>Genetics</i> , 2004 , 166, 389-417	4	305
262	Complete nucleotide sequence and organization of the atrazine catabolic plasmid pADP-1 from <i>Pseudomonas</i> sp. strain ADP. <i>Journal of Bacteriology</i> , 2001 , 183, 5684-97	3.5	303
261	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. <i>Nucleic Acids Research</i> , 1991 , 19, 6553-8	20.1	294
260	A new resource for cereal genomics: 22K barley GeneChip comes of age. <i>Plant Physiology</i> , 2004 , 134, 960-8	6.6	266
259	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D1028-33	30.1	262
258	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014 , 46, 982-8	36.3	259
257	JOINTLESS is a MADS-box gene controlling tomato flower abscission zone development. <i>Nature</i> , 2000 , 406, 910-3	50.4	253
256	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995 , 7, 175-184	6.9	253
255	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14349-54	11.5	247
254	Rate variation among nuclear genes and the age of polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003 , 20, 633-43	8.3	246
253	Promoter analysis of genes that are coordinately expressed during pollen development reveals pollen-specific enhancer sequences and shared regulatory elements. <i>Genes and Development</i> , 1991 , 5, 496-507	12.6	245
252	Isolation and expression of an anther-specific gene from tomato. <i>Molecular Genetics and Genomics</i> , 1989 , 217, 240-5		237
251	Physical and genetic structure of the maize genome reflects its complex evolutionary history. <i>PLoS Genetics</i> , 2007 , 3, e123	6	234
250	In-depth view of structure, activity, and evolution of rice chromosome 10. <i>Science</i> , 2003 , 300, 1566-9	33.3	234
249	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018 , 50, 285-296	36.3	229
248	Functional genomics of cell elongation in developing cotton fibers. <i>Plant Molecular Biology</i> , 2004 , 54, 911-29	4.6	216
247	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016 , 17, 37	18.3	213

246	LysM-type mycorrhizal receptor recruited for rhizobium symbiosis in nonlegume Parasponia. <i>Science</i> , 2011 , 331, 909-12	33.3	213
245	Microcolinearity in sh2-homologous regions of the maize, rice, and sorghum genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 3431-5	11.5	206
244	Genome dynamics and evolution of the Mla (powdery mildew) resistance locus in barley. <i>Plant Cell</i> , 2002 , 14, 1903-17	11.6	201
243	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007 , 17, 175-83	9.7	200
242	A detailed RFLP map of <i>Sorghum bicolor</i> x <i>S. propinquum</i> , suitable for high-density mapping, suggests ancestral duplication of <i>Sorghum</i> chromosomes or chromosomal segments. <i>Theoretical and Applied Genetics</i> , 1994 , 87, 925-33	6	200
241	Aluminum tolerance in maize is associated with higher MATE1 gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5241-6	11.5	199
240	The Mla (powdery mildew) resistance cluster is associated with three NBS-LRR gene families and suppressed recombination within a 240-kb DNA interval on chromosome 5S (1HS) of barley. <i>Genetics</i> , 1999 , 153, 1929-48	4	196
239	A rapid procedure for the isolation of C0t-1 DNA from plants. <i>Genome</i> , 1997 , 40, 138-42	2.4	188
238	<i>Hamiltonella defensa</i> , genome evolution of protective bacterial endosymbiont from pathogenic ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9063-8	11.5	187
237	The <i>Oryza</i> bacterial artificial chromosome library resource: construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Research</i> , 2006 , 16, 140-7	9.7	177
236	A bacterial artificial chromosome library for barley (<i>Hordeum vulgare</i> L.) and the identification of clones containing putative resistance genes. <i>Theoretical and Applied Genetics</i> , 2000 , 101, 1093-1099	6	177
235	A conserved repetitive DNA element located in the centromeres of cereal chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 14210-3	11.5	172
234	Construction and characterization of a bovine bacterial artificial chromosome library. <i>Genomics</i> , 1995 , 29, 413-25	4.3	168
233	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013 , 4, 46	6.2	156
232	Rice transposable elements: a survey of 73,000 sequence-tagged-connectors. <i>Genome Research</i> , 2000 , 10, 982-90	9.7	152
231	Toward a cytological characterization of the rice genome. <i>Genome Research</i> , 2001 , 11, 2133-41	9.7	151
230	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017 , 8, 1279	17.4	149
229	Extensive sequence divergence between the reference genomes of two elite indica rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E5163-71	11.5	141

228	Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. <i>Extremophiles</i> , 2012 , 16, 553-66	3	139
227	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , 2005 , 3, 20	7.3	139
226	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017 , 45, D1075-D1081	10.1	137
225	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018 , 19, 505-517	30.1	135
224	Molecular and genetic characterization of two pollen-expressed genes that have sequence similarity to pectate lyases of the plant pathogen <i>Erwinia</i> . <i>Plant Molecular Biology</i> , 1990 , 14, 17-28	4.6	135
223	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013 , 4, 1595	17.4	132
222	The oryza map alignment project: the golden path to unlocking the genetic potential of wild rice species. <i>Plant Molecular Biology</i> , 2005 , 59, 53-62	4.6	130
221	Structure and architecture of the maize genome. <i>Plant Physiology</i> , 2005 , 139, 1612-24	6.6	130
220	Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13206-11	11.5	129
219	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006 , 16, 441-50	9.7	126
218	High-resolution pachytene chromosome mapping of bacterial artificial chromosomes anchored by genetic markers reveals the centromere location and the distribution of genetic recombination along chromosome 10 of rice. <i>Genetics</i> , 2001 , 157, 1749-57	4	126
217	The Rice Paradox: Multiple Origins but Single Domestication in Asian Rice. <i>Molecular Biology and Evolution</i> , 2017 , 34, 969-979	8.3	124
216	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015 , 5, 15655	4.9	124
215	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007 , 23, 134-9	8.5	118
214	A single molecule scaffold for the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000711	6	110
213	Changes in regulation of a transcription factor lead to autogamy in cultivated tomatoes. <i>Science</i> , 2007 , 318, 643-5	33.3	109
212	The International Oryza Map Alignment Project: development of a genus-wide comparative genomics platform to help solve the 9 billion-people question. <i>Current Opinion in Plant Biology</i> , 2013 , 16, 147-56	9.9	108
211	Integrative transformation of the yeast <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1985 , 10, 39-48	2.9	106

210	The barley ERF-type transcription factor HvRAF confers enhanced pathogen resistance and salt tolerance in Arabidopsis. <i>Planta</i> , 2007 , 225, 575-88	4.7	105
209	Dynamic evolution of oryza genomes is revealed by comparative genomic analysis of a genus-wide vertical data set. <i>Plant Cell</i> , 2008 , 20, 3191-209	11.6	104
208	Evolution of a complex locus for terpene biosynthesis in solanum. <i>Plant Cell</i> , 2013 , 25, 2022-36	11.6	103
207	Genetic, physical, and informatics resources for maize. On the road to an integrated map. <i>Plant Physiology</i> , 2002 , 130, 1598-605	6.6	100
206	Comparative population genetics of the panicoid grasses: sequence polymorphism, linkage disequilibrium and selection in a diverse sample of sorghum bicolor. <i>Genetics</i> , 2004 , 167, 471-83	4	97
205	Fluorescent in situ hybridization of a bacterial artificial chromosome. <i>Genome</i> , 1995 , 38, 646-51	2.4	97
204	Construction and characterization of two rice bacterial artificial chromosome libraries from the parents of a permanent recombinant inbred mapping population. <i>Molecular Breeding</i> , 1996 , 2, 11	3.4	97
203	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006 , 16, 1241-51	11.5	95
202	Comparative sequence analysis of MONOCULM1-orthologous regions in 14 Oryza genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2071-6	11.5	94
201	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017 , 3, 17064	11.5	91
200	Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction. <i>Plant Physiology</i> , 2005 , 138, 105-15	6.6	91
199	Access to the Maize Genome: An Integrated Physical and Genetic Map. <i>Plant Physiology</i> , 2002 , 128, 9-12	6.6	90
198	A bacterial artificial chromosome library for sugarcane. <i>Theoretical and Applied Genetics</i> , 1999 , 99, 419-24	1.4	90
197	An improved method for plant BAC library construction. <i>Methods in Molecular Biology</i> , 2003 , 236, 3-20	1.4	89
196	Diploid/polyploid syntenic shuttle mapping and haplotype-specific chromosome walking toward a rust resistance gene (Bru1) in highly polyploid sugarcane (2n approximately 12x approximately 115). <i>Genetics</i> , 2008 , 180, 649-60	4	88
195	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization. <i>Plant Physiology</i> , 2004 , 134, 1317-26	6.6	88
194	Efficient insertional mutagenesis in rice using the maize En/Spm elements. <i>Plant Journal</i> , 2005 , 44, 879-92	9.2	87
193	Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004 , 32, 2023-30	20.1	86

192	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015 , 5, 17394	4.9	85
191	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2007 , 52, 342-51	6.9	85
190	Transposable element distribution, abundance and role in genome size variation in the genus <i>Oryza</i> . <i>BMC Evolutionary Biology</i> , 2007 , 7, 152	3	84
189	The physical and genetic framework of the maize B73 genome. <i>PLoS Genetics</i> , 2009 , 5, e1000715	6	83
188	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon Fusarium wilt (Fom-2). <i>Genome</i> , 2001 , 44, 154-162	2.4	83
187	Making a living while starving in the dark: metagenomic insights into the energy dynamics of a carbonate cave. <i>ISME Journal</i> , 2014 , 8, 478-91	11.9	82
186	Genomic and genetic characterization of rice Cen3 reveals extensive transcription and evolutionary implications of a complex centromere. <i>Plant Cell</i> , 2006 , 18, 2123-33	11.6	82
185	Whole-genome validation of high-information-content fingerprinting. <i>Plant Physiology</i> , 2005 , 139, 27-386.6		81
184	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021 , 184, 1156-1170.e14	56.2	81
183	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015 , 102, 1115-27	2.7	80
182	Assembly and validation of the genome of the nonmodel basal angiosperm <i>Amborella</i> . <i>Science</i> , 2013 , 342, 1516-7	33.3	79
181	Species trees from highly incongruent gene trees in rice. <i>Systematic Biology</i> , 2009 , 58, 489-500	8.4	79
180	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018 , 16, 1904-1917	11.6	77
179	Resolution of fluorescence in-situ hybridization mapping on rice mitotic prometaphase chromosomes, meiotic pachytene chromosomes and extended DNA fibers. <i>Chromosome Research</i> , 2002 , 10, 379-87	4.4	77
178	Toward integration of comparative genetic, physical, diversity, and cytomolecular maps for grasses and grains, using the sorghum genome as a foundation. <i>Plant Physiology</i> , 2001 , 125, 1325-41	6.6	77
177	Construction, alignment and analysis of twelve framework physical maps that represent the ten genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008 , 9, R45	18.3	72
176	Incongruent patterns of local and global genome size evolution in cotton. <i>Genome Research</i> , 2004 , 14, 1474-82	9.7	71
175	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014 , 5, 5269	17.4	69

174	Construction and characterization of a bacterial artificial chromosome library of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 1995 , 13, 124-128	1.7	69
173	Candidate gene database and transcript map for peach, a model species for fruit trees. <i>Theoretical and Applied Genetics</i> , 2005 , 110, 1419-28	6	68
172	The Wild Relative of Rice: Genomes and Genomics 2013 , 9-25		67
171	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (<i>Gossypium</i>). <i>Plant Journal</i> , 2007 , 50, 995-1006	6.9	67
170	Gene-based SSR markers for common bean (<i>Phaseolus vulgaris</i> L.) derived from root and leaf tissue ESTs: an integration of the BMc series. <i>BMC Plant Biology</i> , 2011 , 11, 50	5.3	66
169	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005 , 15, 1284-91	9.7	66
168	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon Fusarium wilt (Fom-2). <i>Genome</i> , 2001 , 44, 154-162	2.4	66
167	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019 , 29, 870-880	9.7	62
166	Dasheng: a recently amplified nonautonomous long terminal repeat element that is a major component of pericentromeric regions in rice. <i>Genetics</i> , 2002 , 161, 1293-305	4	62
165	Sorghum expressed sequence tags identify signature genes for drought, pathogenesis, and skotomorphogenesis from a milestone set of 16,801 unique transcripts. <i>Plant Physiology</i> , 2005 , 139, 869-84	6.6	61
164	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017 , 3, e1602382	14.3	60
163	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon RIRE1 within the genus <i>Oryza</i> . <i>Plant Journal</i> , 2008 , 53, 950-9	6.9	60
162	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017 , 1, 119	12.3	59
161	A fine physical map of the rice chromosome 4. <i>Genome Research</i> , 2002 , 12, 817-23	9.7	58
160	Profiling bacterial diversity and taxonomic composition on speleothem surfaces in Kartchner Caverns, AZ. <i>Microbial Ecology</i> , 2013 , 65, 371-83	4.4	57
159	Localization of jointless-2 gene in the centromeric region of tomato chromosome 12 based on high resolution genetic and physical mapping. <i>Theoretical and Applied Genetics</i> , 2004 , 108, 190-6	6	57
158	A bacterial artificial chromosome library for soybean PI 437654 and identification of clones associated with cyst nematode resistance. <i>Plant Molecular Biology</i> , 1999 , 41, 25-32	4.6	57
157	Gene identification in a complex chromosomal continuum by local genomic cross-referencing. <i>Plant Journal</i> , 1996 , 10, 1163-8	6.9	57

156	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015 , 16, 538	4.5	56
155	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016 , 2, 16167	11.5	56
154	Deep and comparative analysis of the mycelium and appressorium transcriptomes of Magnaporthe grisea using MPSS, RL-SAGE, and oligoarray methods. <i>BMC Genomics</i> , 2006 , 7, 310	4.5	54
153	Cloning and characterization of a centromere-specific repetitive DNA element from Sorghum bicolor. <i>Theoretical and Applied Genetics</i> , 1998 , 96, 832-839	6	53
152	The Amborella genome: an evolutionary reference for plant biology. <i>Genome Biology</i> , 2008 , 9, 402	18.3	52
151	A versatile transposon-based activation tag vector system for functional genomics in cereals and other monocot plants. <i>Plant Physiology</i> , 2008 , 146, 189-99	6.6	52
150	Physical mapping of the rice genome with BACs 1997 , 35, 115-127		51
149	Construction of a bacterial artificial chromosome library from the spikemoss Selaginella moellendorffii: a new resource for plant comparative genomics. <i>BMC Plant Biology</i> , 2005 , 5, 10	5.3	51
148	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 12003-12008	11.5	50
147	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009 , 2, 35-43	5.8	50
146	Rapid evolution of protein diversity by de novo origination in Oryza. <i>Nature Ecology and Evolution</i> , 2019 , 3, 679-690	12.3	49
145	A large-insert (130 kbp) bacterial artificial chromosome library of the rice blast fungus Magnaporthe grisea: genome analysis, contig assembly, and gene cloning. <i>Fungal Genetics and Biology</i> , 1997 , 21, 337-47	3.9	49
144	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (Phaseolus vulgaris L.) Genome. <i>Tropical Plant Biology</i> , 2008 , 1, 40-48	1.6	49
143	Australian Oryza: Utility and Conservation. <i>Rice</i> , 2010 , 3, 235-241	5.8	48
142	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. <i>Genome</i> , 2008 , 51, 294-302	2.4	48
141	In-depth sequence analysis of the tomato chromosome 12 centromeric region: identification of a large CAA block and characterization of pericentromere retrotransposons. <i>Chromosoma</i> , 2005 , 114, 103-117	2.8	48
140	Access to the maize genome: an integrated physical and genetic map. <i>Plant Physiology</i> , 2002 , 128, 9-12	6.6	48
139	Single Nucleotide Polymorphisms and InsertionDeletions for Genetic Markers and Anchoring the Maize Fingerprint Contig Physical Map. <i>Crop Science</i> , 2006 , 46, 12-21	2.4	47

138	New resources for marine genomics: bacterial artificial chromosome libraries for the Eastern and Pacific oysters (<i>Crassostrea virginica</i> and <i>C. gigas</i>). <i>Marine Biotechnology</i> , 2006 , 8, 521-33	3.4	47
137	Comparative gene expression in sexual and apomictic ovaries of <i>Pennisetum ciliare</i> (L.) Link. <i>Plant Molecular Biology</i> , 1996 , 32, 1085-92	4.6	47
136	The Genomics of Species Provides Insights into Rice Domestication and Heterosis. <i>Annual Review of Plant Biology</i> , 2019 , 70, 639-665	30.7	46
135	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019 , 10, 4680	17.4	45
134	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). <i>BMC Genomics</i> , 2010 , 11, 395	4.5	45
133	Evaluation of genetic variation in the daylily (<i>Hemerocallis</i> spp.) using AFLP markers. <i>Theoretical and Applied Genetics</i> , 2001 , 102, 489-496	6	44
132	Physical mapping of the liguleless linkage group in <i>Sorghum bicolor</i> using rice RFLP-selected sorghum BACs. <i>Genetics</i> , 1998 , 148, 1983-92	4	44
131	Ginger and turmeric expressed sequence tags identify signature genes for rhizome identity and development and the biosynthesis of curcuminoids, gingerols and terpenoids. <i>BMC Plant Biology</i> , 2013 , 13, 27	5.3	43
130	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010 , 63, 430-42	6.9	43
129	RL-SAGE and microarray analysis of the rice transcriptome after <i>Rhizoctonia solani</i> infection. <i>Molecular Genetics and Genomics</i> , 2007 , 278, 421-31	3.1	43
128	Comparative physical mapping between <i>Oryza sativa</i> (AA genome type) and <i>O. punctata</i> (BB genome type). <i>Genetics</i> , 2007 , 176, 379-90	4	42
127	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021 , 590, 438-444	5.4	42
126	An integrated physical, genetic and cytogenetic map of <i>Brachypodium distachyon</i> , a model system for grass research. <i>PLoS ONE</i> , 2010 , 5, e13461	3.7	41
125	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. <i>Functional and Integrative Genomics</i> , 2004 , 4, 102-17	3.8	40
124	Development of genomic resources for cotton (<i>Gossypium hirsutum</i> L.): BAC library construction, preliminary STC analysis, and identification of clones associated with fiber development. <i>Molecular Breeding</i> , 2001 , 8, 255-261	3.4	40
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